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EC-11775.DNA 25: ACACCGGTCAACATTGAGGAAGAGCTGAAGAGCTCCTATCTGGATTATGCGATGTCGGTC
 CF-8090.DNA
 EA-13048.DNAG.....A.....G.....
 ECL13047.DNAT.....C.....C.....
 KO-13182.DNA
 KP-13883.DNAT...A...T.....
 PS-29914.DNAT.C.A....A.C.A..T.G..T.....C..T
 SM-13880.DNAA....C..A..C...T...A.A..G.....C.....C..T
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EC-11775.DNA 85: ATTGTTGGCCGTGCGCTGCCAGATGTCCGAGATGGCCTGAAGCCGGTACACCGTCGCGTA
 CF-8090.DNAC.....T.....
 EA-13048.DNAG.....
 ECL13047.DNAG.C....C.....
 KO-13182.DNAG.....
 KP-13883.DNAG.....
 PS-29914.DNAC.G..C....T.....T.....A.....A.....CA.A..
 SM-13880.DNAC..A....C.....T..T....A.....T....C....T
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EC-11775.DNA 145: CTTTACGCCATGAACGTACTAGGCAATGACTGGAACAAAGCCTATAAAAAATCTGCCCGT
 CF-8090.DNAT.G....C.....T.....
 EA-13048.DNA ..A.....T.G.....A.....
 ECL13047.DNA ..A.....T.G.....T.....C.....
 KO-13182.DNA ..A.....T.G.....A.....
 KP-13883.DNAT.G.....
 PS-29914.DNA ..G.TT..G....T..T.G..A....T....T..C.....
 SM-13880.DNA ..G....G....G....T.G..T..C.....T..C.A..C..G....G.....
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EC-11775.DNA 205: GTCGTTGGTGACGTAATCGGTAAATACCATCCCCATGGTGACTCGCGGTTTATGACACG
 CF-8090.DNAC..T.....TA.C..C....C....C
 EA-13048.DNAC.....C.G.....TA.C..C....C
 ECL13047.DNAT..C....G..C....C
 KO-13182.DNAG.....C.....C..T.....TA.T..C..A..C....C
 KP-13883.DNAC.G..C..C....C....A..C....C
 PS-29914.DNA A.A..C..G....T.....A.....TAGC..T.....G..A
 SM-13880.DNAC..G....G.....T..C..G..C....AGC.....C....T
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EC-11775.DNA 265: ATCGTCCGTATGGCGCAGCCATTCTCGCTGCGTTACATGCTGGTAGACGGTCAGGGTAAC
 CF-8090.DNA ..T..T.....CT.....T.....
 EA-13048.DNAA.....G....CT.....T.....C..T..C.....
 ECL13047.DNAT.....T.....T.....
 KO-13182.DNA ..T..A.....C.....T..C.....
 KP-13883.DNAG.....G.....G....C.....
 PS-29914.DNAT..C.T..T....T..T..TA.....T.....T.....G..
 SM-13880.DNAG.....T....G..T..A....C.....G.....
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Fig - 1A

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EC-11775.DNA 325: TTCGGTTCCATCGACGGCGACTCTCGGGCGGCAATGCGTTATACGGAAATCCGTCTGGCG
CF-8090.DNA ..T.....TG....T.....C..A.....G.....A..T..
EA-13048.DNA ..T.....TG....T.....C..T..A..G.....A..T..
ECL13047.DNA ..T.....T.....C..C.....A..T..
KO-13182.DNA ..T.....GG.....C..C..A..G.....A..T..
KP-13883.DNA ..T.....C.....C.....G.....C.....T.....
PS-29914.DNA ..T.....AG.T....A..T..C..A..T.....A.....
SM-13880.DNAG.....C.....G.....C..G..G..CA..T.C
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EC-11775.DNA 385: AAAATTGCCCATGAACTGATGGCTGATCTCGAAAAAGAGACGGTCGATTTCGTTGATAAC
CF-8090.DNAC.....G.....C..G.....A.....T.....C.....
EA-13048.DNA ..G..C..T.....G.....C.....T.....C..C..
ECL13047.DNAG.....C..C..G.....T.....
KO-13182.DNA ..G..C.....C..C.....G.....C.....
KP-13883.DNAC..T.....G.....C.....T.....C..C..
PS-29914.DNAA..T..A..G.....C..T.....CCCA..
SM-13880.DNA ..G.....T..C.....T.....G.....A..C.....GCC..
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EC-11775.DNA 445: TATGACGGTACGGAAAAAATTCGGGACGTCATGCCAACCAAAATTCCTAACCTGCTGGTG
CF-8090.DNA ..C.....C..C..C.....T.....G.....
EA-13048.DNAC.....G.....C..T.....G..A.....C.....
ECL13047.DNA ..C..T..C.....T.....G..G..C.....
KO-13182.DNAC.....G.....C..T.....T.....G.....C..G.....A..C
KP-13883.DNAGCGT.....G.....
PS-29914.DNAT.....A..GC...C..T..A..T.....T..G.....C.....AT...T
SM-13880.DNAT..C..C..GC..G..C.....C.....G.....G..C..G.....C
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EC-11775.DNA 505: AACGGTTCTTCCGGTATCGCCGTAGGTATGGCAACCAACATCCCGCCGCACAACCTGACG
CF-8090.DNAG.....G.....T.....T.....
EA-13048.DNAG.....G.....T.....T.....
ECL13047.DNAG.....G.....G.....T.....A..C..C
KO-13182.DNAG.....G.....G..T..T..T.....C
KP-13883.DNACG..C.....G.....G.....C.....A.....A..T.....
PS-29914.DNA ..T.....G..A.....T..T..T..G.....G.....T..T..A.....AGG.
SM-13880.DNAC..G..G..C.....G..C.....T.....T..T.....G..
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EC-11775.DNA 565: GAAGTCATCAACGGTTGTCTGGCGTATATCGATGATGAAGACATCAGCA
CF-8090.DNAG.....C.....A.....T..C.....
EA-13048.DNAT.....C..C.....A..CG.T...A.C.....
ECL13047.DNAG.....C..C.....C.....C.....
KO-13182.DNAG.....C.....C..CG.T..AA.C.....
KP-13883.DNAG..T.....C.....G..T..C.....
PS-29914.DNAG...G.....C..T..T.....A.....T..T..
SM-13880.DNAG.....C..C.....C.....C.....A.....
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Fig - 1B

DNase Sequence Similarity of the QDR⁺ in Enterobacteriaceae

199	S83	258
<i>E. coli</i> **	GCCCGTGTGGTGACGTAAATCGGTAAATACCATCCCATGGTGACTCGGCGGTTTAT	
<i>C. freundii</i>C.T.....TA.C.C.....C	
<i>E. aerogenes</i>C.....C.G.....TA.C.C.....	
<i>E. cloacae</i>T.C.....G.C	
<i>K. oxytoca</i>G.....C.T.....TA.T.C.A.C	
<i>K. pneumoniae</i>C.G.C.C.....C.....A.C	
<i>P. stuartii</i>A.A.C.G.....T.....TAGC.T.....	
<i>S. marcescens</i>C.G.....G.....T.C.G.C.....AGC.....C	
	***** ** ** ** ***** ** ** ** **	***** ** ** **

259	GACACGATCGTCGGTATGGCGGACGCCATTCTCGTGGTTACATGCTGCTAGACGGTCAG	318
<i>E. coli</i>C.T.T.....CT.....T.....	
<i>C. freundii</i>C.....A.....G.....CT.....C.T.C...	
<i>E. aerogenes</i>C.....T.....T.....T.....C.T.C...	
<i>E. cloacae</i>C.T.A.....C.....C.....T.C...	
<i>K. oxytoca</i>C.....G.....G.....G.....G.C...	
<i>K. pneumoniae</i>G.A.....T.C.T.T.T.TA.....T.....T...	
<i>P. stuartii</i>T.....G.....T.....G.T.A.....G.....	
<i>S. marcescens</i>	*** ** ** ** **	*** ** ** ** *

* Yoshida et al., 1990. Antimicrob. Agents Chemother. 34:1271.
* Swanberg and Wang, 1987. J. Mol. Biol. 197:729.

Similarity of the Amino Acid Sequences of the QRDR
of Enterobacteriaceae

	67	83	87	106
<i>E. coli</i>	ARVVG	VDVIGKYHPHG	DSAVYDTIV	RMQPFSLRYMLVDGQ
<i>C. freundii</i>T.....
<i>E. aerogenes</i>T.....
<i>E. cloacae</i>
<i>K. oxytoca</i>T.....
<i>K. pneumoniae</i>
<i>P. stuartii</i>	I.....E.....	L.....	M.....
<i>S. marcescens</i>	**	**	**	**

Fig. 3

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Strain	MIC ($\mu\text{g/ml}$) ¹			Amino acid change ²		
	CIP	OFLX	SPAR	81	GyrA 83	87 (codon)
<i>C. freundii</i>						
ATCC 8090	≤ 0.12	≤ 0.25	≤ 0.008	Gly (GGT)	Thr (ACC)	Asp (GAC)
Cf 7377	2	8	>2	-	Ile (ATC)	-
Cf 0759	2	8	>2	-	Ile (ATC)	-
Cf 9085	4	8	2	-	Ile (ATC)	-
Cf 9417	8	8	>2	-	Ile (ATC)	-
Cf 1958	≥ 16	≥ 16	>2	-	Ile (ATC)	Gly (GGC)
Cf 5757	≥ 16	≥ 16	>2	-	Ile (ATC)	Gly (GGC)
Cf 9023	≥ 16	≥ 16	>2	-	Ile (ATC)	-
<i>E. aerogenes</i>						
ATCC 13048	0.5	1	0.25	Gly (GGT)	Thr (ACC)	Asp (GAC)
Ea 1747	≤ 0.12	<0.25	0.06	-	-	-
Ea 2786	2	4	2	-	Ile (ATC)	-
Ea 9032	4	4	2	-	Ile (ATC)	-
Ea 5593	8	8	>2	-	Ile (ATC)	-
Ea 9433	8	≥ 16	>2	-	Ile (ATC)	-
Ea 3521	8	≥ 16	>2	-	Ile (ATC)	-
Ea 5590	8	≥ 16	>2	-	Ile (ATC)	-
Ea 2775	≥ 16	32	>2	-	Ile (ATC)	-
<i>E. cloacae</i>						
ATCC 13047	≤ 0.12	≤ 0.25	0.03	Gly (GGT)	Ser (TCC)	Asp (GAC)
Ecl 1700	≤ 0.12	<0.25	0.06	-	-	-
Ecl 1524	0.25	0.5	0.12	-	-	Asn (AAC)
Ecl 1963	2	4	2	-	Phe (TTC)	-
Ecl 1286	2	4	1	-	Tyr (TAC)	-
Ecl 3529	4	8	>2	-	Thr (ACC)	-
Ecl 1544	8	8	>2	-	Tyr (TAC)	-
Ecl 1627	8	≥ 16	>2	-	Tyr (TAC)	-
Ecl 9028	≥ 16	8	>2	-	Ile (ATC)	-
Ecl 1224	≥ 16	8	>2	-	Phe (TTC)	Asn (AAC)
Ecl 1251	≥ 16	≥ 16	>2	-	Ile (ATC)	-
Ecl 63	≥ 16	≥ 16	>2	-	Phe (TTC)	-
Ecl 105	≥ 16	≥ 16	>2	-	Phe (TTC)	-
Ecl 1783	≥ 16	≥ 16	>2	-	Tyr (TAC)	-
Ecl 9030	≥ 16	≥ 16	>2	-	Tyr (TAC)	-
Ecl 9031	≥ 16	>32	>2	-	Ile (ATC)	-
<i>E. coli</i>						
ATCC 11775	≤ 0.12	≤ 0.25	0.03	Gly (GGT)	Ser (TCG)	Asp (GAC)
Ec 748	≤ 0.12	≤ 0.25	0.03	-	-	-
Ec 3535	1	2	2	-	Leu (TTG)	-
Ec 5524	2	8	2	-	Leu (TTG)	-
Ec 9419	≥ 16	32	>2	-	Leu (TTG)	Gly (GGA)
Ec 9421	≥ 16	32	>2	-	Leu (TTG)	Tyr (TAC)
Ec 9425	≥ 16	>32	>2	-	Leu (TTG)	Asn (AAC)



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Strain	MIC ($\mu\text{g/ml}$)			Amino acid change		
	CIP	OFLX	SPAR	81	GyrA 83	87 (codon)
<i>K. pneumoniae</i>						
ATCC 13883	0.5	≤ 0.25	0.06	Gly (GGC)	Ser (TCC)	Asp (GAC)
Kp 570	≤ 0.12	≤ 0.25	0.06	-	-	-
Kp 1961	≤ 0.12	≤ 0.25	0.03	-	-	-
Kp 2778	≤ 0.12	≤ 0.25	0.03	-	-	-
Kp 2790	≤ 0.12	≤ 0.25	0.03	-	-	-
Kp 1361	1	2	0.5	-	Phe (TTC)	-
Kp 1362	1	2	1	-	Phe (TTC)	-
Kp 1177	4	≥ 16	> 2	-	Phe (TTC)	-
Kp 682	≥ 16	≥ 16	> 2	-	Phe (TTC)	-
Kp 1768	≥ 16	32	> 2	-	Tyr (TAC)	-
Kp 1775	≥ 16	> 32	> 2	-	Phe (TTC)	Gly (GGC)
Kp 1565	≥ 16	> 32	> 2	-	Tyr (TAC)	Asn (AAC)
<i>K. oxytoca</i>						
ATCC 13182	≤ 0.12	≤ 0.25	0.12	Gly (GGT)	Thr (ACT)	Asp (GAC)
Ko 702	≤ 0.12	≤ 0.25	0.03	-	-	-
Ko 2538	≤ 0.12	≤ 0.25	0.06	-	-	-
Ko 2110	≤ 0.12	≤ 0.25	0.06	-	-	-
Ko 1199	≤ 0.12	≤ 0.25	0.06	-	-	-
Ko 57	0.5	0.05	0.25	-	Ile (ATT)	-
Ko 1577	4	4	2	-	Ile (ATT)	-
Ko 1817	8	≥ 16	> 2	-	Ile (ATT)	-
Ko 466	≥ 16	8	> 2	-	Ile (ATT)	-
Ko 32	≥ 16	≥ 16	> 2	-	Ile (ATT)	-
Ko 1578	≥ 16	≥ 16	> 2	-	Ile (ATT)	-
Ko 1612	≥ 16	≥ 16	> 2	-	Ile (ATT)	-
Ko 2777	≥ 16	> 32	> 2	-	Ile (ATT)	-
<i>P. stuartii</i>						
ATCC 29914	≤ 0.12	≤ 0.25	≤ 0.12	Gly (GGT)	Ser (AGC)	Glu (GAG)
Ps 1571	0.25	1	0.5	-	-	-
Ps 1284	2	4	2	-	Arg (CGC)	-
Ps 2469	8	≥ 16	> 2	-	Ile (ATC)	-
Ps 2783	≥ 16	≥ 16	2	-	Arg (AGG)	-
Ps 9428	≥ 16	≥ 16	> 2	-	Ile (ATC)	-
Ps 7375	≥ 16	32	> 2	-	Ile (ATC)	-
Ps 2468	≥ 16	32	> 2	-	Ile (ATC)	-
Ps 1773	≥ 16	> 32	> 2	-	Arg (AGG)	-
<i>S. marcescens</i>						
ATCC 13880	0.5	1	1	Gly (GGT)	Ser (AGC)	Asp (GAC)
Sm 1714	0.25	1	1	-	-	-
Sm 9745	2	4	2	-	Ile (ATC)	-
Sm 1221	4	8	> 2	Cys (TGT)	-	-
Sm 1969	4	≥ 16	> 2	-	-	Asn (AAC)
Sm 1570	8	8	> 2	Cys (TGT)	-	-
Sm 5591	8	≥ 16	> 2	-	Arg (AGA)	-
Sm 1568	≥ 16	≥ 16	> 2	-	Arg (CGC)	-

¹ CIP, ciprofloxacin; OFLX, ofloxacin; SPAR, sparfloxacin² -, identical to the ATCC type strain
